Figure 1

Gene symbol	Gene name
OSBP	Oxysterol-binding protein
NFKB3 (p65)	nuclear factor of kappa light polypeptide gene enhancer B-cells 3
CAPN1	Calpain, large polypeptide L1
CCND1	Cyclin D1
EFEMP2*	EGF-containing fibulin-like extracellular matrix protein 2
FOSL1	FOS-like antigen-1
PLCB3	Phospholipase C, beta 3 (phosphatidylinositol-specific)
PPP1CA	Protein phosphatase-1, catalytic subunit, alpha isoform
VEGFB	Vascular endothelial growth factor B
ESRRA, ERR1	estrogen-related receptor alpha
CTSW	Cathepsin W
GALN*	Galanin
LRP5, LRP7, LR3*	Low density lipoprotein receptor-related protein-5
CBP2	Collagen-binding protein 2 (colligen 2)
TCIRG1	T-cell immune regulator 1
LTBP3	Latent transforming growth factor-beta binding protein-3
FGF19*	Fibroblast growth factor 19 (FGF19)
Delta5-desaturase*	Delta5-desaturase

Figure 2

```
    GCCATGGAGCCCGAGTGAGCGCGGCGCGGGCCCGTCCGGCCGCCGGACAACAT
    GGAGGCAGCGCCGCCCGGGCCGCCGTGGCCGCTGCTGCTGCTGCTGCTGCTGCT
 5  GCTGGCGCTGTGCGGCTGCCCGGCCCCCGCCGCGGCCTCGCCGCTCCTGCTATTT
    GCCAACCGCCGGGACGTACGGCTGGTGGACGCCGGCGGAGTCAAGCTGGAGTC
    CACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGCAGTGGACTTCCAGTTTTC
    CAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCT
    ACCTGAACCAGACGGGGGCCGCCGTGCAGAACGTGGTCATCTCCGGCCTGGTCT
10  CTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACT
    CAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGC
    TCTTCTGGCAGGACCTTGACCAGCCTAGGGCCATCGCCTTGGACCCCGCTCACG
    GGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGG
    ATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAAT
15  GGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACTGGGCTGACGCCAAGCTC
    AGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAG
    GGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGG
    ACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAG
    AGGAAGGAGATCCTGAGTGCCCTCTACTCACCCATGGACATCCAGGTGCTGAGC
20  CAGGAGCGGCAGCCTTTCTTCCACACTCGCTGTGAGGAGGACAATGGCGGCTGC
    TCCCACCTGTGCCTGCTGTCCCCAAGCGAGCCTTTCTACACATGCGCCTGCCCCA
    CGGGTGTGCAGCTGCAGGACAACGGCAGGACGTGTAAGGCAGGAGCCGAGGAG
    GTGCTGCTGCTGGCCCGGCGGACGGACCTACGGAGGATCTCGCTGGACACGCCG
    GACTTCACCGACATCGTGCTGCAGGTGGACGACATCCGGCACGCCATTGCCATC
25  GACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGTGCGGGCC
    ATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGAG
    ATCAACGACCCCGATGGCATCGCGGTCGACTGGGTGGCCCGAAACCTCTACTGG
    ACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGC
    AAGATCCTGGTGTCGGAGGACCTGGACGAGCCCCGAGCCATCGCACTGCACCCC
30  GTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCCTAAAATCGAGTGT
    GCCAACTTGGATGGGCAGGAGCGGCGTGTGCTGGTCAATGCCTCCCTCGGGTGG
    CCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCTCTACTGGGGAGACGCC
    AAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACCCT
    CCTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCAT
35  CTACTGGACTGACTGGCAGCGCCGCAGCATCGAGCGGGTGCACAAGGTCAAGGC
    CAGCCGGGACGTCATCATTGACCAGCTGCCCGACCTGATGGGGCTCAAAGCTGT
    GAATGTGGCCAAGGTCGTCGGAACCAACCCGTGTGCGGACAGGAACGGGGGGT
    GCAGCCACCTGTGCTTCTTCACACCCCACGCAACCCGGTGTGGCTGCCCCATCG
    GCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGG
40  TCTTCACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACG
    ACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATG
    TGTCCAACAACCACATCTACTGGACAGACGTCAGCCTGAAGACCATCAGCCGCG
    CCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCTTGACTACC
    CCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTG
45  GGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTC
    GTGTGGAGGGACTTGGACAACCCGAGGTCGCTGGCCCTGGATCCCACCAAGGGC
    TACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATG
```

Figure 2 (Page 2 of 3)

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    GACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCCGGGCCAACGACCT
    CACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACAT
    GATCGAGTCGTCCAACATGCTGGGTCAGGAGCGGGTCGTGATTGCCGACGATCT
    CCCGCACCCGTTCGGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTG
  5 GAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCT
    CATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCACTCCTCCCGC
    CAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGC
    CTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGAC
    CCCAGCAGCCGCAACTGCAGCCCGCCCACCACCTTCTTGCTGTTCAGCCAGAAA
 10 TCTGCCATCAGTCGGATGATCCCGGACGACCAGCACAGCCCGGATCTCATCCTG
    CCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAG
    TTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAGGACGACGG
    GACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAGGCCAAAACCCAGACAGGCA
    GCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGA
 15 GGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGG
    TGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAACGCGGAGCGA
    GGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCA
    GCCCTGGACGGCACCGAGCGCGAGGTCCTCTTCACCACCGGCCTCATCCGCCCT
    GTGGCCCTGGTGGTGGACAACACACTGGGCAAGCTGTTCTGGGTGGACGCGGAC
 20 CTGAAGCGCATTGAGAGCTGTGACCTGTCAGGGGCCAACCGCCTGACCCTGGAG
    GACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTAC
    TGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGA
    CAAGCGGACTCGCATCCAGGGCCGTGTCGCCCACCTCACTGGCATCCATGCAGT
    GGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCACCCATGTGCCCGTGACAATGG
 25 TGGCTGCTCCCACATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATG
    CCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCCAC
    CTGCTCCCCGGACCAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGG
    GGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGG
    CTGCCCCGTGTGCTCCGCCGCCCAGTTCCCCTGCGCGCGGGGTCAGTGTGTGGA
 30 CCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGC
    GGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTG
    TGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGA
    CGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCGGCCCACAG
    CAGTGCCATCGGGCCCGTCATTGGCATCATCCTCTCTCTCTTCGTCATGGGTGGT
 35 GTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAACGGG
    CCCTTCCCGCACGAGTATGTCAGCGGGACCCCGCACGTGCCCCTCAATTTCATA
    GCCCCGGGCGGTTCCCAGCATGGCCCCTTCACAGGCATCGCATGCGGAAAGTCC
    ATGATGAGCTCCGTGAGCCTGATGGGGGGCCGGGGCGGGGTGCCCCTGTACGAC
    CGGAACCACGTCACAGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACG
 40 CTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTG
    TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTAC
    AGGCCCTACATCATTCGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGAC
    GTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTG
    GATTTGAACTCGGACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAG
 45 TACCTGTCGGCGGAGGACAGCTGCCCGCCCTCGCCCGCCACCGAGAGGAGCTAC
    TTCCATCTCTTCCCGCCCCCTCCGTCCCC
    CTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCTG
    TAAATAGTTTTAAATATGAACAAAGAAAAAAATATATTTTATGATTTAAAAAAT
```

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AAATATAATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGC
AGGGCTGGGAGAACTTTGTA

Figure 3

MEAAPPGPPWPLLLLLLLLLLALCGCPAPAAASPLLLFANRRDVRLVDAGGVKLESTI
VVSGLEDAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTGAAVQNVVISGLVSPDGL
ACDWVGKKLYWTDSETNRIEVANLNGTSRKVLFWQDLDQPRAIALDPAHGYMYW
TDWGETPRIERAGMDGSTRKIIVDSDIYWPNGLTIDLEEQKLYWADAKLSFIIHRANL
DGSFRQKVVEGSLTHPFALTLSGDTLYWTDWQTRSIHACNKRTGGKRKEILSALYSP
MDIQVLSQERQPFFHTRCEEDNGGCSHLCLLSPSEPFYTCACPTGVQLQDNGRTCKA
GAEEVLLLARRTDLRRISLDTPDFTDIVLQVDDIRHAIAIDYDPLEGYVYWTDDEVR
AIRRAYLDGSGAQTLVNTEINDPDGIAVDWVARNLYWTDTGTDRIEVTRLNGTSRK
ILVSEDLDEPRAIALHPVMGLMYWTDWGENPKIECANLDGQERRVLVNASLGWPN
GLALDLQEGKLYWGDAKTDKIEVINVDGTKRRTLLEDKLPHIFGFTLLGDFIYWTD
WQRRSIERVHKVKASRDVIIDQLPDLMGLKAVNVAKVVGTNPCADRNGGCSHLCFF
TPHATRCGCPIGLELLSDMKTCIVPEAFLVFTSRAAIHRISLETNNNDVAIPLTGVKE
ASALDFDVSNNHIYWTDVSLKTISRAFMNGSSVEHVVEFGLDYPEGMAVDWMGKN
LYWADTGTNRIEVARLDGQFRQVLVWRDLDNPRSLALDPTKGYTYWTEWGGKPRI
VRAFMDGTNCMTLVDKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLGQERVV
IADDLPHPFGLTQYSDYIYWTDWNLHSIERADKTSGRNRTLIQGHLDFVMDILVFHS
SRQDGLNDCMHNNGQCGQLCLAIPGGHRCGCASHYTLDPSSRNCSPPTTFLLFSQKS
AISRMIPDDQHSPDLILPLHGLRNVKAIDYDPLDKFIYWVDGRQNIKRAKDDGTQPF
VLTSLSQGQNPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLSGEAMGVVLRGDRDK
PRAIVVNAERGYLYFTNMQDRAAKIERAALDGTEREVLFTTGLIRPVALVVDNTLG
KLFWVDADLKRIESCDLSGANRLTLEDANIVQPLGLTILGKHLYWIDRQQQMIERVE
KTTGDKRTRIQGRVAHLTGIHAVEEVSLEEFSAHPCARDNGGCSHICIAKGDGTPRC
SCPVHLVLLQNLLTCGEPPTCSPDQFACATGEIDCIPGAWRCDGFPECDDQSDEEGC
PVCSAAQFPCARGQCVDLRLRCDGEADCQDRSDEADCDAICLPNQFRCASGQCVLI
KQQCDSFPDCIDGSDELMCEITKPPSDDSPAHSSAIGPVIGIILSLFVMGGVYFVCQRV
VCQRYAGANGPFPHEYVSGTPHVPLNFIAPGGSQHGPFTGIACGKSMMSSVSLMGG
RGGVPLYDRNHVTGASSSSSSSTKATLYPPILNPPPSPATDPSLYNMDMFYSSNIPAT
ARPYRPYIIRGMAPPTTPCSTDVCDSDYSASRWKASKYYLDLNSDSDPYPPPPTPHSQ
YLSAEDSCPPSPATERSYFHLFPPPPSPCTDSS

Figure 4

Source	Nucleotide change	Protein change	Putative effect
OPS 88	G29A	Trp10stop	Truncation
Control	A459G	Pro153Pro	No change
Control	InsCTG33	Insert Leu at residue 12	Alters signal peptide
OPS 78	GACCTACG 1051-1058 ACCCTACA	AspLeuSer 351-353 ThrLeuLys	Unknown
OPS 59	C1282T	Arg428stop	Truncation
OPS 53	G1253T	Glu485stop	Truncation
OPS 23	delG1467	Frameshift	Truncation
OPS 82	G1481A	Arg494Gln	Unknown
OPS 2	C1708T	Arg570Trp	Unknown
OPS 72	G1999A	Val677Met	Unknown
OPS 45	insT2150	Frameshift	Truncation
OPS 41	G2202A	Trp734stop	Unknown
Control	C2220T	Asn740Asn	Unknown
OPS 92	delG2305	Frameshift	Truncation
OPS13	C2557T	Gln853stop	Truncation
OPS 7	delA3804	Frameshift	Truncation
OPS 53	C3989T	Ala1330Leu	Unknown
OPS 72	C3989T	Ala1330Leu	Unknown
Control	G4416T	Leu1472Leu	No change

5

Figure 5

NAME	SEQUENCE	LOCATION	PRODUCT SIZE
LRGEN1F	5'-TTG CTG CCC TAG ACT TAG CC-3'	-119	406
LRGEN1R	5'-CCA AGT CGC TTC CGA GAC-3'	+106	
LRGEN2F	5'-CAT CCC AGG GCT GTG TAT CT-3'	-65	543
LRGEN2R	5'-ACT TGG GCT CAT GCA AAT TC-3'	+81	
LRGEN3F1	5'-CCG ATG GGT GAG ATT TTA GG-3'	-118	329
LRGEN3R1	5'-CGT GGG TAC CTA CCG GAA C-3'	+16	
LRGEN4NF	5'-TAA TTG GGT CAG CAG CAA TG-3'	-72	277
LRGEN4NR	5'-GCA CTC ACA GAA AGG CTG-3'	+8	
LRGEN5NF	5'-AGT GAC GGT CCT CTT CTG GA-3'	-51	302
LRGEN5NR	5'-CAA GTG GAT CAT TTC GAA CG-3'	+120	
LRGEN6F	5'-TGG CTG AGT ATT TCC CTT GC-3'	-95	577
LRGEN6R	5'-CCA GAA TGA CAG GTC CAG GT-3'	+85	
LRGEN7F1	5'-TGC TTC TTC TCC AGC CTC AT-3'	-14	302
LRGEN7R1	5'-ATG TGG CCA AAT AGC AGA GC-3'	+116	
LRGEN8F	5'-GCA TTG AAC CCG TCT TGT TT-3'	-109	426
LRGEN8R	5'-GGC ACC TGA GCT CAA CAC TT-3'	+100	
LRGEN9F	5'-TGC TGG GCT GTT GT GTT TA-3'	-47	407
LRGEN9R	5'-CTT TGA GGC AGG AAC AGA GG-3'	+70	
LRGEN10F	5'-AGC GAA ACT CCG TCT CAA AA-3'	-79	417
LRGEN10R	5'-GCT CTA ATC ACT GAG GGC CA-3'	+110	
LRGEN11F1	5'-GAG GGC TGA GCT GAA GAG GT-3'	-105	398
LRGEN11R1	5'-CAG GTT GGG GAA CTT GCA G-3'	+108	
LRGEN12F	5'-ATT CAT GTG GTC GCT AGG CT-3'	-113	479
LRGEN12R	5'-GAA GCT CCT TTC AGC GTC AG-3'	+40	
LRGEN13F	5'-CCA GCT CCT CTG TGG CTT AC-3'	-57	352
LRGEN13R	5'-TCC TCC CTC TGC TAA GGA CA-3'	+95	
LRGEN14F	5'-CAG AGC TCT CCA GCC AGT G-3'	-149	440
LRGEN14R	5'-CTG TGA GAG GCT GGC ATT C-3'	+82	
LRGEN15NF	5'-ATG TGA CCT GTC AGC CTC G-3'	-131	415
LRGEN15NR	5'-TGC TGC CAT TAC TGA CAA TGA-3'	+83	
LRGEN16F	5'-TCT GTC CTC CCA AGC TGA GT-3'	-76	374
LRGEN16R	5'-CAC ACA GGA TCT TGC ACT GG-3'	+88	
LRGEN17F	5'-CAT GAG TTC TCA TTT GGC CC-3'	-92	321
LRGEN17R	5'-GCC ACA GGG ACT GTG ATT TT-3'	+103	
LRGEN18F	5'-CAA CTT CTG CTT TGA AGC CC-3'	-88	423
LRGEN18R	5'-CAG AGC CCC TAC TCC TGT GA-3'	+98	
LRGEN19F	5'-CCA GAC CTT GGT TGC TGT G-3'	-81	269
LRGEN19R	5'-CGT CTC CTC CCC TAA ACT CC-3'	+77	
LRGEN20NF	5'-ATG TTG GCC ACC TCT TTC TG-3'	-34	310
LRGEN20NR	5'-CTG CCT CCT CCA GAT CAT TC-3'	+39	
LRGEN21F	5'-GAG TCT CGT GGG TAG TGG GA-3'	-102	373

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LRGEN21R	5'AGA AAG CAA GCA TGC CTC AG-3'	+131	
LRGEN22F	5'-AGC CCT CTC TGC AAG GAA AG-3'	-96	305
LRGEN22R	5'-GCC CAC TAG CAC CCA GAA TA-3'	+111	
LRGEN23F	5'-GAC AGG CCT TTC CCG TTC-3'	-95	650
LRGEN23R	5'-CAG GAG GAC TCT CAT GGT GG-3'	+106	
LRCOD1F	5'-TTC GTC ATG GGT GGT GTC TA-3'	4192	416
LRCOD1R	5'-TTC CTC GAA TGA TGT AGG GC-3'	4607	
LRCOD2F	5'-ACC TGG ACT TCG TGA TGG AC-3'	2654	466
LRCOD2R	5'-CAG AAC AGT GTC CGG CTG TA-3'	3119	
LRCOD3F	5'-CCA TGG AGC CCG AGT GAG-3'	-50	504
LRCOD3R	5'-GTC AAG GTC CTG CCA GAA GA-3'	453	
LRCOD4F	5'-GGG CAA GAA GCT GTA CTG GA-3'	354	500
LRCOD4R	5'-TGG ATG TCC ATG GGT GAG TA-3'	853	
LRCOD5F	5'-CAG ACC CGC TCC ATC CAT-3'	767	484
LRCOD5R	5'-TCG TTG ATC TCG GTG TTG AC-3'	1250	
LRCOD6F	5'-ATC GAC TAC GAC CCG CTA GA-3'	1132	546
LRCOD6R	5'-GTA GAT GAA GTC CCC CAG CA-3'	1677	
LRCOD7F	5'-GCC AAG ACA GAC AAG ATC GAG-3'	1564	505
LRCOD7R	5'-TGT GGT TGT TGG ACA CAT CA-3'	2068	
LRCOD8F	5'-CAC AGG ATC TCC CTC GAG AC-3'	1966	522
LRCOD8R	5'-CTC GAT CAT GTT GGT GTC CA-3'	2487	
LRCOD9F	5'-CAG CCC TTT GTT TTG ACC TC-3'	3025	484
LRCOD9R	5-TCC AGT AGA GAT GCT TGC CA-3'	3508	
LRCOD10F	5'-AAG CGC ATT GAG AGC TGT G-3'	3400	480
LRCOD10R	5'-CTC CTC GTC GCT CTG GTC-3'	3879	
LRCOD11F	5'-CAC AGG GGA GAT CGA CTG TAT-3'	3801	480
LRCOD11R	5'-ACA TAC TCG TGC GGG AAG G-3'	4280	
LRCOD12F	5'-GTC CAG CAG CTC GTC CAG-3'	4446	567
LRCOD12R	5'-TAC AAA GTT CTC CCA GCC CT-3'	5012	
LRCOD13F	5'-TCA TGG ACG GGA CCA ACT-3'	2369	431
LRCOD13R	5'-GGT GTA GTG TGA GGC GCA G-3'	2799	

Figure 6

BMSR Construct Information

5   The following BSMR expression constructs have been constructed using the pcDNA3
expression vector for use in following BSMR expression, function, and other biological
(e.g. ligand and downstream signaling) interactions.

   1.   A full length wild type construct extending from primers LRCOD3F to
10   LRCOD12R.

Sequence encoding a FLAG antibody epitope (GAC TAC AAG GAC GAC GAT GAC
AAG) was inserted into the wild-type construct immediately downstream of nucleotide 165
(relative to the "A" in the ATG translation start site). This construct expresses a BSMR
15   protein which has a FLAG epitope between wild type BSMR amino acid residues 55 and
56.

This was accomplished using the following primer sequences and a Quickchange reaction:

20   LRPFLAGF: 5'-GAC TAC AAG GAC GAC GAT GAC AAG ACC ATC GTG GTC AGC
GGC CTG-3'

LRPFLAGR.5'-CTT GTC ATC GTC GTC CTT GTA GGA CTC CAG CTT GAC TCC
GCC-3'
25

Sequence encoding a MYC antibody epitope (GAG CAG AAG CTG ATA TCC GAG GAG
GAC CTG) was inserted immediately uptream of the stop codon after residue 4845 (relative
to the "A" in the ATG translation start site). The construct expresses a BSMR protein
which has a MYC epitope at the end of the wild type BSMR polypeptide.
30

This was accomplished using the following primer sequences and a Quickchange reaction:

 LRPMYCF: 5'-GAG CAG AAG CTG ATA TCC GAG GAG GAC CTG TGA CCT CGG
CCG GGC-3'
35

LRPMYCR: 5'-CAG GTC CTC CTC GGA TAT CAG CTT CTG CTC GGA TGA GTC
CGT GCA-3'

A expresssion construct containing both the FLAG and MYC antibody epitopes at the
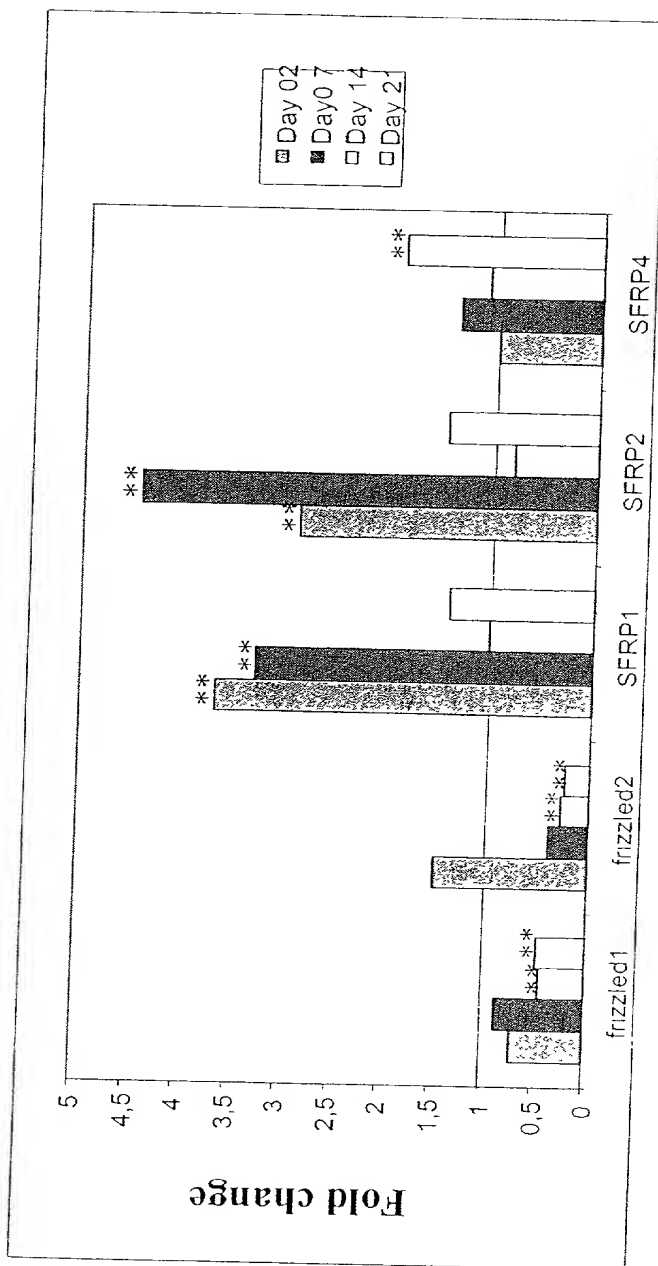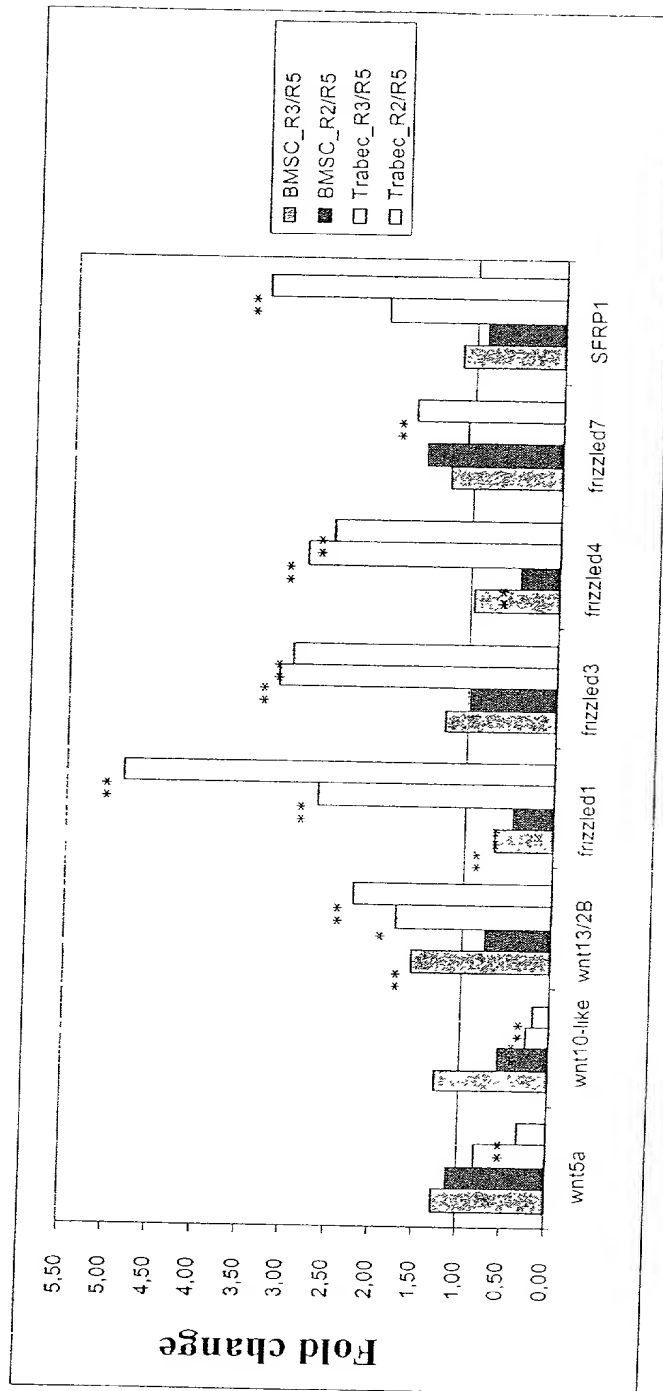40   aforementioned sites has also been produced.

Figure 7

Figure 8

Figure 9

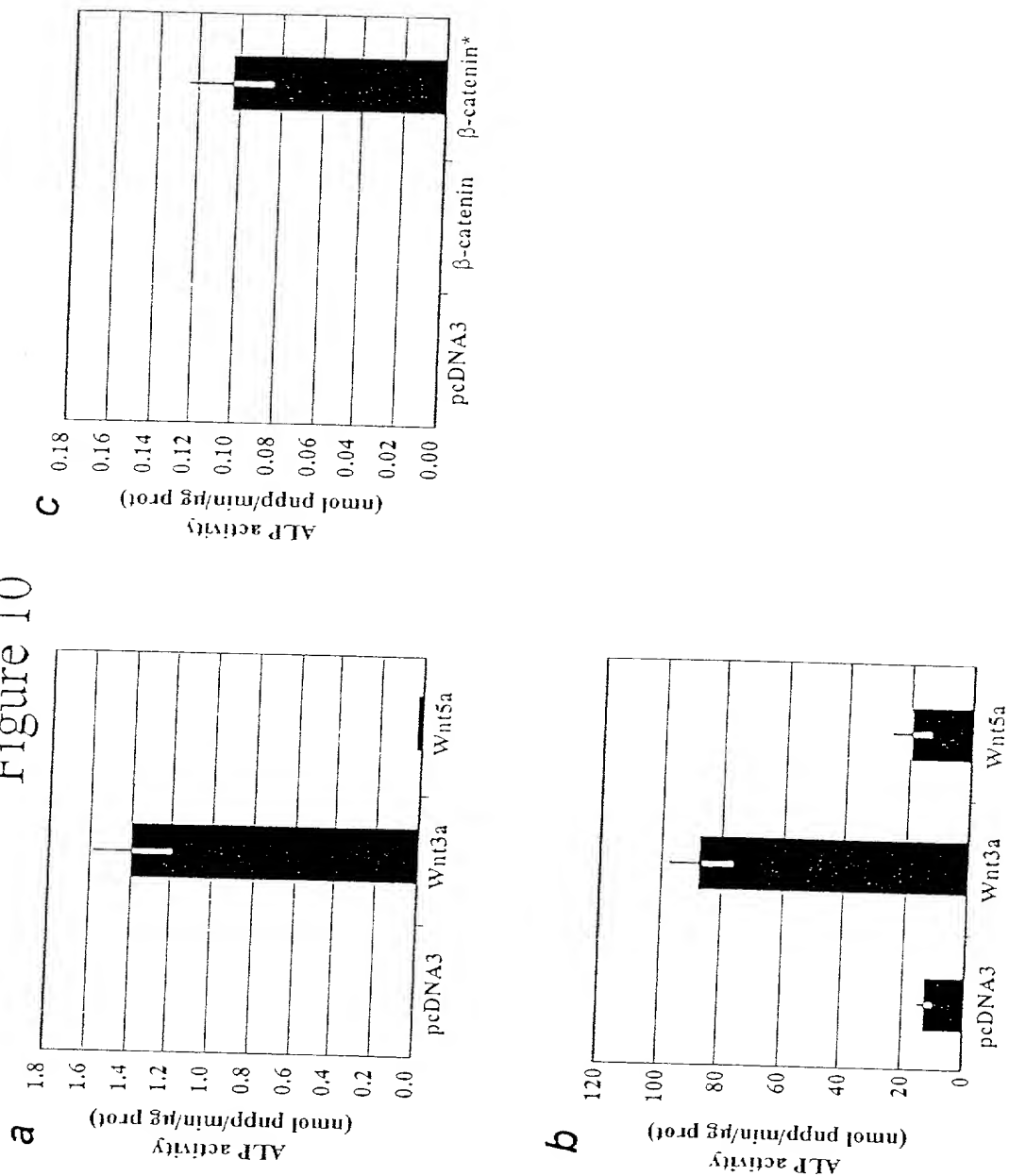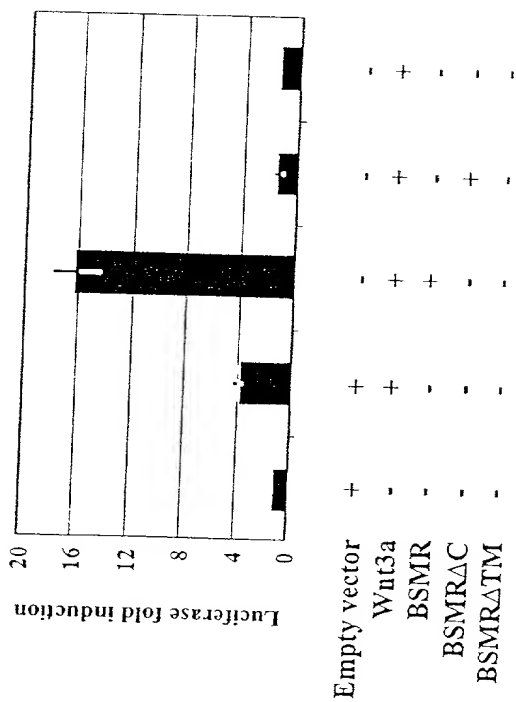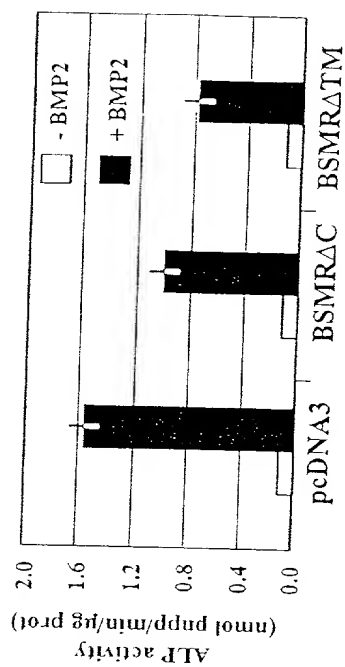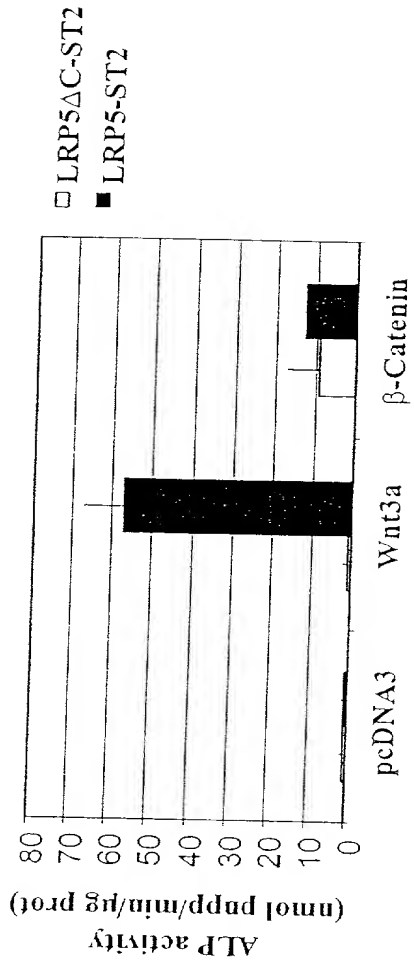| Cell line/treatment Gene name	C2C12/BMP2 (4 days)	C3H10T1/2/BMP2+SHH (4 days)	ST2/BMP2 (4 days)	MC3T3-E1 (3 days)
Frizzled-1	2.25 x	NR	2.62x	2.11x
Frizzled-4	NR	4.37x	NR	NR
SFRP2/SARP1	8.10 x	0.5x (0.4x with SHH alone)	8.54x	3.61x (0.09 with TGFbeta)

Figure 10

Figure 11
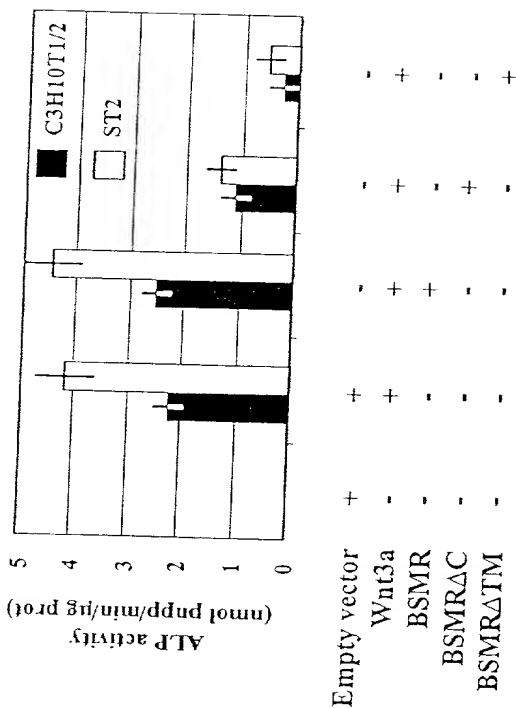
Figure 12

Figure 13

RVRLASHLRKLRK

RLTRKRGLKLA

CRAKRNNFKSA

LKWKS

KIRVKAGETQKKVIFCSREKVSHL

FIPLKPTVKMLERSNHVSRTEVSSNHV

DKGMAPALRHLYKELMGPWN

DALKLAIDNALSIT